```
CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: HrpW                     424 aa
Sequence 2: HopPtoA_SEQIDNO7         486 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:   6
Guide tree        file created:    [/ebi/extserv/old-work/199548.12283.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                    Delayed
Sequence:2      Score:3175
Alignment Score 3
CLUSTAL-Alignment file created  [/ebi/extserv/old-work/199548.12283.aln]
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199548.12283.aln

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CLUSTAL W (1.82) multiple sequence alignment


HrpW              MSIGITPRPQQTTTPLDFSALSGKSPQPNTFGEQNTQQAIDPSALLFGSDTQKDVNFGTP 60
HopPtoA_SEQIDNO7  MHINRRVQQPPVTATDSFRTASDASLASSSVRSVSSDQQREINAIADYLTDHVFAAHKLP 60
                  * *.      :     .*:. .* : *. *  ..:. . .::*   : .*:       :  . . *


HrpW              DSTVQNPQDASKPNDSQSNIAKLISALIMSLLQMLTNSNKKQDTNQEQPDSQAPFQNNGG 120
HopPtoA_SEQIDNO7  PADSADGQAAVDVHNAQITALIETRASRLHFEGETPATIADTFAKAEKLDRLATTTSGAL 120
                  :     : * * . .:::* .      *   : :    . :   .  :: *: *  *. ...


HrpW              LGTPSADSGGGGTPDATGGGG--------GDTPSATGGGGGDTPTATGGGGSGGGGTPTA 172
HopPtoA_SEQIDNO7  RATPFAMASLLQYMQPAINKGDWLPAPLKPLTPLISGALSGAMDQVGTKMMDRATGDLHY 180
                  .** * :.      :.: . *        ** :*. .*       .     . . *


HrpW              TGGGSGGTPTATGGGEGGVTPQITPQLANP-------NRTSGTGSVSDTAGSTEQAGKIN 225
HopPtoA_SEQIDNO7  LSASPDRLHDAMAASVKRHSPSLARQVLDTGVAVQTYSARNAVRTVLAPALASRPAVQGA 240
                  .....        *  ...   :*.:: *: :.      . ...:*  .* ::. * :


HrpW              VVKDTIKVGAGEVFDGHGATFTADKSMGNGDQG------ENQKPMFELAEG-------AT 272
HopPtoA_SEQIDNO7  VDLGVSMAGGLAANAGFGNRLLSVQSRDHQRGGALVLGLKDKEPKAQLSEENDWLEAYKA 300
                  *   ..  .*.  .  *.*  : : :*  .:  *        :::*  :*:*        :


HrpW              LKNVNLGENEVDG-------IHVKAKNAQEVTIDNVHAQNVGEDLITVKG--EGGAAVTN 323
HopPtoA_SEQIDNO7  IKSASYSGAALNAGKRMAGLPLDMATDAMGAVRSLVSASSLTQNGLALAGGFAGVGKLQE 360
                  :*... .  ::.        *.:*  .. . * *..: :: ::: *   *  . : :


HrpW              LNIKNSSAKGADDKVVQLN------------------ANTHLKIDNFKADDFGTMVRTN 364
HopPtoA_SEQIDNO7  MATKNITDPATKAAVSQLTNLAGSAAVFAGWTTAALTTDPAVKKAESFIQDTVKSTASST 420
                  :  ** :  .:.  * **.               :  * :.*  *  . : . .:.


HrpW              GGKQFDDMSIELNGIEANHGKFALVKSDSDDLKLATGNIAMTDVKHAYDKTQASTQHTEL 424
HopPtoA_SEQIDNO7  TG-YVADQTVKLAKTVKDMGGEAITHTGASLRNTVNNLRQRPAREADIEEGGTAASPSEI 479
                    *  . * :::*       : *  *:..:.. : ...   . :     ::  ::::. :*:


HrpW              -------
HopPtoA_SEQIDNO7  PFRPMRS 486
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199548.12283.dnd

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(HrpW:0.46698,HopPtoA_SEQIDNO7:0.46698)
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